RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _____ 10/584,364 _____

Source: _____ IFWP _____

Date Processed by STIC: _____ 07/07/2006 _____

ENTERED

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         3 <110> APPLICANT: Kinch, Michael S.
         5 <120> TITLE OF INVENTION: EphA2 VACCINES
         7 <130> FILE REFERENCE: 10271-148-999
C-->     9 <140> CURRENT APPLICATION NUMBER: US/10/584,364
C-->     9 <141> CURRENT FILING DATE: 2006-06-23
         9 <150> PRIOR APPLICATION NUMBER: US 60/532,696
        10 <151> PRIOR FILING DATE: 2003-12-24
        12 <150> PRIOR APPLICATION NUMBER: US 60/602,588
        13 <151> PRIOR FILING DATE: 2004-08-18
        15 <150> PRIOR APPLICATION NUMBER: US 60/615,548
        16 <151> PRIOR FILING DATE: 2004-10-01
        18 <150> PRIOR APPLICATION NUMBER: US 60/617,564
        19 <151> PRIOR FILING DATE: 2004-10-07
        21 <160> NUMBER OF SEQ ID NOS: 72
        23 <170> SOFTWARE: PatentIn version 3.2
        25 <210> SEQ ID NO: 1
        26 <211> LENGTH: 3963
        27 <212> TYPE: DNA
        28 <213> ORGANISM: Homo sapiens
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        32 <221> NAME/KEY: CDS
        33 <222> LOCATION: (138)..(3068)
        35 <400> SEQUENCE: 1
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        38 accgaggccg gcgtgcaggc gtgcgggtgt gcgggagccg ggctcggggg gatcggaccg    120
        40 agagcgagaa gcgcggc atg gag ctc cag gca gcc cgc gcc tgc ttc gcc       170
        41                    Met Glu Leu Gln Ala Ala Arg Ala Cys Phe Ala
        42                     1               5                  10
        44 ctg ctg tgg ggc tgt gcg ctg gcc gcg gcc gcg gcg gcg cag ggc aag    218
        45 Leu Leu Trp Gly Cys Ala Leu Ala Ala Ala Ala Ala Ala Gln Gly Lys
        46              15                  20                  25
        48 gaa gtg gta ctg ctg gac ttt gct gca gct gga ggg gag ctc ggc tgg    266
        49 Glu Val Val Leu Leu Asp Phe Ala Ala Ala Gly Gly Glu Leu Gly Trp
        50          30                  35                  40
        52 ctc aca cac ccg tat ggc aaa ggg tgg gac ctg atg cag aac atc atg    314
        53 Leu Thr His Pro Tyr Gly Lys Gly Trp Asp Leu Met Gln Asn Ile Met
        54      45                  50                  55
        56 aat gac atg ccg atc tac atg tac tcc gtg tgc aac gtg atg tct ggc    362
        57 Asn Asp Met Pro Ile Tyr Met Tyr Ser Val Cys Asn Val Met Ser Gly
        58 60                  65                  70                  75
        60 gac cag gac aac tgg ctc cgc acc aac tgg gtg tac cga gga gag gct    410
        61 Asp Gln Asp Asn Trp Leu Arg Thr Asn Trp Val Tyr Arg Gly Glu Ala
        62              80                  85                  90
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 64 gag cgt atc ttc att gag ctc aag ttt act gta cgt gac tgc aac agc      458
 65 Glu Arg Ile Phe Ile Glu Leu Lys Phe Thr Val Arg Asp Cys Asn Ser
 66          95              100              105
 68 ttc cct ggt ggc gcc agc tcc tgc aag gag act ttc aac ctc tac tat      506
 69 Phe Pro Gly Gly Ala Ser Ser Cys Lys Glu Thr Phe Asn Leu Tyr Tyr
 70          110              115              120
 72 gcc gag tcg gac ctg gac tac ggc acc aac ttc cag aag cgc ctg ttc      554
 73 Ala Glu Ser Asp Leu Asp Tyr Gly Thr Asn Phe Gln Lys Arg Leu Phe
 74          125              130              135
 76 acc aag att gac acc att gcg ccc gat gag atc acc gtc agc agc gac      602
 77 Thr Lys Ile Asp Thr Ile Ala Pro Asp Glu Ile Thr Val Ser Ser Asp
 78 140              145              150                  155
 80 ttc gag gca cgc cac gtg aag ctg aac gtg gag gag cgc tcc gtg ggg      650
 81 Phe Glu Ala Arg His Val Lys Leu Asn Val Glu Glu Arg Ser Val Gly
 82              160              165              170
 84 ccg ctc acc cgc aaa ggc ttc tac ctg gcc ttc cag gat atc ggt gcc      698
 85 Pro Leu Thr Arg Lys Gly Phe Tyr Leu Ala Phe Gln Asp Ile Gly Ala
 86              175              180              185
 88 tgt gtg gcg ctg ctc tcc gtc cgt gtc tac tac aag aag tgc ccc gag      746
 89 Cys Val Ala Leu Leu Ser Val Arg Val Tyr Tyr Lys Lys Cys Pro Glu
 90          190              195              200
 92 ctg ctg cag ggc ctg gcc cac ttc cct gag acc atc gcc ggc tct gat      794
 93 Leu Leu Gln Gly Leu Ala His Phe Pro Glu Thr Ile Ala Gly Ser Asp
 94          205              210              215
 96 gca cct tcc ctg gcc act gtg gcc ggc acc tgt gtg gac cat gcc gtg      842
 97 Ala Pro Ser Leu Ala Thr Val Ala Gly Thr Cys Val Asp His Ala Val
 98 220              225              230                  235
100 gtg cca ccg ggg ggt gaa gag ccc cgt atg cac tgt gca gtg gat ggc      890
101 Val Pro Pro Gly Gly Glu Glu Pro Arg Met His Cys Ala Val Asp Gly
102              240              245              250
104 gag tgg ctg gtg ccc att ggg cag tgc ctg tgc cag gca ggc tac gag      938
105 Glu Trp Leu Val Pro Ile Gly Gln Cys Leu Cys Gln Ala Gly Tyr Glu
106              255              260              265
108 aag gtg gag gat gcc tgc cag gcc tgc tcg cct gga ttt ttt aag ttt      986
109 Lys Val Glu Asp Ala Cys Gln Ala Cys Ser Pro Gly Phe Phe Lys Phe
110          270              275              280
112 gag gca tct gag agc ccc tgc ttg gag tgc cct gag cac acg ctg cca     1034
113 Glu Ala Ser Glu Ser Pro Cys Leu Glu Cys Pro Glu His Thr Leu Pro
114          285              290              295
116 tcc cct gag ggt gcc acc tcc tgc gag tgt gag gaa ggc ttc ttc cgg     1082
117 Ser Pro Glu Gly Ala Thr Ser Cys Glu Cys Glu Glu Gly Phe Phe Arg
118 300              305              310                  315
120 gca cct cag gac cca gcg tcg atg cct tgc aca cga ccc ccc tcc gcc     1130
121 Ala Pro Gln Asp Pro Ala Ser Met Pro Cys Thr Arg Pro Pro Ser Ala
122              320              325              330
124 cca cac tac ctc aca gcc gtg ggc atg ggt gcc aag gtg gag ctg cgc     1178
125 Pro His Tyr Leu Thr Ala Val Gly Met Gly Ala Lys Val Glu Leu Arg
126              335              340              345
128 tgg acg ccc cct cag gac agc ggg ggc cgc gag gac att gtc tac agc     1226
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129 Trp Thr Pro Pro Gln Asp Ser Gly Gly Arg Glu Asp Ile Val Tyr Ser
130     350                 355                 360
132 gtc acc tgc gaa cag tgc tgg ccc gag tct ggg gaa tgc ggg ccg tgt   1274
133 Val Thr Cys Glu Gln Cys Trp Pro Glu Ser Gly Glu Cys Gly Pro Cys
134     365                 370                 375
136 gag gcc agt gtg cgc tac tcg gag cct cct cac gga ctg acc cgc acc   1322
137 Glu Ala Ser Val Arg Tyr Ser Glu Pro Pro His Gly Leu Thr Arg Thr
138 380                 385                 390                 395
140 agt gtg aca gtg agc gac ctg gag ccc cac atg aac tac acc ttc acc   1370
141 Ser Val Thr Val Ser Asp Leu Glu Pro His Met Asn Tyr Thr Phe Thr
142                 400                 405                 410
144 gtg gag gcc cgc aat ggc gtc tca ggc ctg gta acc agc cgc agc ttc   1418
145 Val Glu Ala Arg Asn Gly Val Ser Gly Leu Val Thr Ser Arg Ser Phe
146         415                 420                 425
148 cgt act gcc agt gtc agc atc aac cag aca gag ccc ccc aag gtg agg   1466
149 Arg Thr Ala Ser Val Ser Ile Asn Gln Thr Glu Pro Pro Lys Val Arg
150         430                 435                 440
152 ctg gag ggc cgc agc acc acc tcg ctt agc gtc tcc tgg agc atc ccc   1514
153 Leu Glu Gly Arg Ser Thr Thr Ser Leu Ser Val Ser Trp Ser Ile Pro
154     445                 450                 455
156 ccg ccg cag cag agc cga gtg tgg aag tac gag gtc act tac cgc aag   1562
157 Pro Pro Gln Gln Ser Arg Val Trp Lys Tyr Glu Val Thr Tyr Arg Lys
158 460                 465                 470                 475
160 aag gga gac tcc aac agc tac aat gtg cgc cgc acc gag ggt ttc tcc   1610
161 Lys Gly Asp Ser Asn Ser Tyr Asn Val Arg Arg Thr Glu Gly Phe Ser
162                 480                 485                 490
164 gtg acc ctg gac gac ctg gcc cca gac acc acc tac ctg gtc cag gtg   1658
165 Val Thr Leu Asp Asp Leu Ala Pro Asp Thr Thr Tyr Leu Val Gln Val
166         495                 500                 505
168 cag gca ctg acg cag gag ggc cag ggg gcc ggc agc aag gtg cac gaa   1706
169 Gln Ala Leu Thr Gln Glu Gly Gln Gly Ala Gly Ser Lys Val His Glu
170         510                 515                 520
172 ttc cag acg ctg tcc ccg gag gga tct ggc aac ttg gcg gtg att ggc   1754
173 Phe Gln Thr Leu Ser Pro Glu Gly Ser Gly Asn Leu Ala Val Ile Gly
174     525                 530                 535
176 ggc gtg gct gtc ggt gtg gtc ctg ctt ctg gtg ctg gca gga gtt ggc   1802
177 Gly Val Ala Val Gly Val Val Leu Leu Leu Val Leu Ala Gly Val Gly
178 540                 545                 550                 555
180 ttc ttt atc cac cgc agg agg aag aac cag cgt gcc cgc cag tcc ccg   1850
181 Phe Phe Ile His Arg Arg Arg Lys Asn Gln Arg Ala Arg Gln Ser Pro
182             560                 565                 570
184 gag gac gtt tac ttc tcc aag tca gaa caa ctg aag ccc ctg aag aca   1898
185 Glu Asp Val Tyr Phe Ser Lys Ser Glu Gln Leu Lys Pro Leu Lys Thr
186         575                 580                 585
188 tac gtg gac ccc cac aca tat gag gac ccc aac cag gct gtg ttg aag   1946
189 Tyr Val Asp Pro His Thr Tyr Glu Asp Pro Asn Gln Ala Val Leu Lys
190         590                 595                 600
192 ttc act acc gag atc cat cca tcc tgt gtc act cgg cag aag gtg atc   1994
193 Phe Thr Thr Glu Ile His Pro Ser Cys Val Thr Arg Gln Lys Val Ile
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194     605                  610                 615
196 gga gca gga gag ttt ggg gag gtg tac aag ggc atg ctg aag aca tcc     2042
197 Gly Ala Gly Glu Phe Gly Glu Val Tyr Lys Gly Met Leu Lys Thr Ser
198 620                 625                 630                 635
200 tcg ggg aag aag gag gtg ccg gtg gcc atc aag acg ctg aaa gcc ggc     2090
201 Ser Gly Lys Lys Glu Val Pro Val Ala Ile Lys Thr Leu Lys Ala Gly
202                 640                 645                 650
204 tac aca gag aag cag cga gtg gac ttc ctc ggc gag gcc ggc atc atg     2138
205 Tyr Thr Glu Lys Gln Arg Val Asp Phe Leu Gly Glu Ala Gly Ile Met
206                 655                 660                 665
208 ggc cag ttc agc cac cac aac atc atc cgc cta gag ggc gtc atc tcc     2186
209 Gly Gln Phe Ser His His Asn Ile Ile Arg Leu Glu Gly Val Ile Ser
210                 670                 675                 680
212 aaa tac aag ccc atg atg atc atc act gag tac atg gag aat ggg gcc     2234
213 Lys Tyr Lys Pro Met Met Ile Ile Thr Glu Tyr Met Glu Asn Gly Ala
214     685                 690                 695
216 ctg gac aag ttc ctt cgg gag aag gat ggc gag ttc agc gtg ctg cag     2282
217 Leu Asp Lys Phe Leu Arg Glu Lys Asp Gly Glu Phe Ser Val Leu Gln
218 700                 705                 710                 715
220 ctg gtg ggc atg ctg cgg ggc atc gca gct ggc atg aag tac ctg gcc     2330
221 Leu Val Gly Met Leu Arg Gly Ile Ala Ala Gly Met Lys Tyr Leu Ala
222                 720                 725                 730
224 aac atg aac tat gtg cac cgt gac ctg gct gcc cgc aac atc ctc gtc     2378
225 Asn Met Asn Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val
226                 735                 740                 745
228 aac agc aac ctg gtc tgc aag gtg tct gac ttt ggc ctg tcc cgc gtg     2426
229 Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Leu Ser Arg Val
230     750                 755                 760
232 ctg gag gac gac ccc gag gcc acc tac acc acc agt ggc ggc aag atc     2474
233 Leu Glu Asp Asp Pro Glu Ala Thr Tyr Thr Thr Ser Gly Gly Lys Ile
234     765                 770                 775
236 ccc atc cgc tgg acc gcc ccg gag gcc att tcc tac cgg aag ttc acc     2522
237 Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ser Tyr Arg Lys Phe Thr
238 780                 785                 790                 795
240 tct gcc agc gac gtg tgg agc ttt ggc att gtc atg tgg gag gtg atg     2570
241 Ser Ala Ser Asp Val Trp Ser Phe Gly Ile Val Met Trp Glu Val Met
242                 800                 805                 810
244 acc tat ggc gag cgg ccc tac tgg gag ttg tcc aac cac gag gtg atg     2618
245 Thr Tyr Gly Glu Arg Pro Tyr Trp Glu Leu Ser Asn His Glu Val Met
246                 815                 820                 825
248 aaa gcc atc aat gat ggc ttc cgg ctc ccc aca ccc atg gac tgc ccc     2666
249 Lys Ala Ile Asn Asp Gly Phe Arg Leu Pro Thr Pro Met Asp Cys Pro
250     830                 835                 840
252 tcc gcc atc tac cag ctc atg atg cag tgc tgg cag cag gag cgt gcc     2714
253 Ser Ala Ile Tyr Gln Leu Met Met Gln Cys Trp Gln Gln Glu Arg Ala
254     845                 850                 855
256 cgc cgc ccc aag ttc gct gac atc gtc agc atc ctg gac aag ctc att     2762
257 Arg Arg Pro Lys Phe Ala Asp Ile Val Ser Ile Leu Asp Lys Leu Ile
258 860                 865                 870                 875
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RAW SEQUENCE LISTING   DATE: 07/07/2006
PATENT APPLICATION: US/10/584,364   TIME: 14:48:54

Input Set : E:\10271-148-999.txt
Output Set: N:\CRF4\07072006\J584364.raw

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260 cgt gcc cct gac tcc ctc aag acc ctg gct gac ttt gac ccc cgc gtg    2810
261 Arg Ala Pro Asp Ser Leu Lys Thr Leu Ala Asp Phe Asp Pro Arg Val
262         880             885             890
264 tct atc cgg ctc ccc agc acg agc ggc tcg gag ggg gtg ccc ttc cgc    2858
265 Ser Ile Arg Leu Pro Ser Thr Ser Gly Ser Glu Gly Val Pro Phe Arg
266         895             900             905
268 acg gtg tcc gag tgg ctg gag tcc atc aag atg cag cag tat acg gag    2906
269 Thr Val Ser Glu Trp Leu Glu Ser Ile Lys Met Gln Gln Tyr Thr Glu
270         910             915             920
272 cac ttc atg gcg gcc ggc tac act gcc atc gag aag gtg gtg cag atg    2954
273 His Phe Met Ala Ala Gly Tyr Thr Ala Ile Glu Lys Val Val Gln Met
274     925             930             935
276 acc aac gac gac atc aag agg att ggg gtg cgg ctg ccc ggc cac cag    3002
277 Thr Asn Asp Asp Ile Lys Arg Ile Gly Val Arg Leu Pro Gly His Gln
278 940             945             950             955
280 aag cgc atc gcc tac agc ctg ctg gga ctc aag gac cag gtg aac act    3050
281 Lys Arg Ile Ala Tyr Ser Leu Leu Gly Leu Lys Asp Gln Val Asn Thr
282         960             965             970
284 gtg ggg atc ccc atc tga gcctcgacag ggcctggagc cccatcggcc           3098
285 Val Gly Ile Pro Ile
286             975
288 aagaatactt gaagaaacag agtggcctcc ctgctgtgcc atgctgggcc actgggggact  3158
290 ttatttattt ctagttcttt cctccccctg caacttccgc tgaggggtct cggatgacac    3218
292 cctggcctga actgaggaga tgaccaggga tgctgggctg ggccctcttt ccctgcgaga    3278
294 cgcacacagc tgagcactta gcaggcaccg ccacgtccca gcatccctgg agcaggagcc    3338
296 ccgccacagc cttcggacag acatatagga tattcccaag ccgaccttcc ctccgccttc    3398
298 tcccacatga ggccatctca ggagatggag ggcttggccc agcgccaagt aaacagggta    3458
300 cctcaagccc catttcctca cactaagagg gcagactgtg aacttgactg ggtgagaccc    3518
302 aaagcggtcc ctgtccctct agtgccttct ttagaccctc gggccccatc ctcatccctg    3578
304 actggccaaa cccttgcttt cctgggcctt tgcaagatgc ttggttgtgt tgaggttttt    3638
306 aaatatatat tttgtacttt gtggagagaa tgtgtgtgtg tggcagggg ccccgccagg     3698
308 gctggggaca gagggtgtca aacattcgtg agctggggac tcaggaccg gtgctgcagg     3758
310 agtgtcctgc ccatgcccca gtcggcccca tctctcatcc ttttggataa gtttctattc    3818
312 tgtcagtgtt aaagattttg ttttgttgga cattttttc gaatcttaat ttattatttt     3878
314 ttttatattt attgttagaa aatgacttat ttctgctctg gaataaagtt gcagatgatt    ·3938
316 caaaccgaaa aaaaaaaaaa aaaaa                                           3963
319 <210> SEQ ID NO: 2
320 <211> LENGTH: 976
321 <212> TYPE: PRT
322 <213> ORGANISM: Homo sapiens
324 <400> SEQUENCE: 2
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330 Ala Leu Ala Ala Ala Ala Ala Ala Gln Gly Lys Glu Val Val Leu Leu
331         20              25              30
334 Asp Phe Ala Ala Ala Gly Gly Glu Leu Gly Trp Leu Thr His Pro Tyr
335         35              40              45
338 Gly Lys Gly Trp Asp Leu Met Gln Asn Ile Met Asn Asp Met Pro Ile
339     50              55              60
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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 07/07/2006
PATENT APPLICATION: US/10/584,364 TIME: 14:48:55

Input Set : E:\10271-148-999.txt
Output Set: N:\CRF4\07072006\J584364.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:66; N Pos. 1

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:22; Line(s) 1200
Seq#:33; Line(s) 2376

VERIFICATION SUMMARY   DATE: 07/07/2006
PATENT APPLICATION: US/10/584,364   TIME: 14:48:55

Input Set : E:\10271-148-999.txt
Output Set: N:\CRF4\07072006\J584364.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:4000 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66 after pos.:0